

## SEQUENCE PROTOCOL

&lt;110&gt; Degussa AG

5 &lt;120&gt; New nucleotide sequences which code for the mikE17 gene

&lt;130&gt; 000561 BT

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 4

&lt;170&gt; PatentIn Ver. 2.1

15

&lt;210&gt; 1

&lt;211&gt; 1890

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

20

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (252)..(1673)

&lt;223&gt; mikE17 gene

25

&lt;400&gt; 1

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cttgcgtag gtgacacaat tatccaaaca gttgcaccgt aggtgcctaa aaagttcccg 120

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gggcggatgt gccccgacca cgccggcac ctggtggcgg cgggctgcgt cgaaaagcga 180

aaatcaacaa gtttgcaaca ctcagtgcc aagagtggg aaggtgatgg tgatcacgct 240

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atagttgcgc c atg gga aag aca tat gtg ggg tcc agg ctg cgc caa ctg 290  
Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu

1

5

10

40

cgc cgc gaa aga gac ctg agc cag gca tcc tta gca gca acc ctt ggc 338  
Arg Arg Glu Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly  
15 20 25

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tta tct gca agt tat gta aat cag att gag cac gac gta cgc ccg ctc 386  
Leu Ser Ala Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu  
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50

acc gta ccg gtg tta ttg cgc atc acc gag gcg ttc ggc gta gac gca 434  
Thr Val Pro Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala  
50 55 60acg ttt ttc tcc cgc gac gat gac tcc cgc ctg ctc gcc gag gtc caa 482  
Thr Phe Phe Ser Arg Asp Asp Ser Arg Leu Leu Ala Glu Val Gln  
65 70 75

55

gac gtc atg ctg gac cgg gag atc aat cct gcg aac gtg gag ctg caa 530  
Asp Val Met Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln  
80 85 90

gag ctt tcg gag atg gtg tac aac cac ccc caa cta gcg cgc gcg atg Glu Leu Ser Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met 95 100 105	578
5 gtg gaa atg cac cag cgt tac cga aac gtg cgc gat aag ttc tcc atc Val Glu Met His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile 110 115 120 125	626
10 gca gtg gat aat cgc acc aac acg cct gag gaa cgc cgt ccc atc gcg Ala Val Asp Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala 130 135 140	674
15 gag gcc gtg agc atg ccg cac gaa gag gtc cgc gat ttc att tac gcc Glu Ala Val Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala 145 150 155	722
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45 gcc acc gaa ctc ggc tac cta gaa gcc aac gac ctc atc gaa ggt atc Ala Thr Glu Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile 240 245 250	1010
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55 cgc ggt gtg gcc tcc tac ttc gcc gcc gtg atg ctg ccc tac aaa Arg Gly Val Ala Ser Tyr Phe Ala Ala Val Met Leu Pro Tyr Lys 270 275 280 285	1106
50 atc ttc cac tcc gag gcc gaa aaa tcc ggc tac gac atc gag tac cta Ile Phe His Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu 290 295 300	1154
55 ggc caa ctc ttt ggc gtg ggc tat gag aca acc gcc cac cgc ttg tcc Gly Gln Leu Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser 305 310 315	1202

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Thr Leu Gln Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg	
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gtc gac cgc gcc ggc aac atg tcc aaa cgc caa tcc gcc acc ggc ttc	1298
Val Asp Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe	
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10 cac ttc acc cac tac ggc ggc acc tgc ccc ctg tgg aac gtg ttt gaa	1346
His Phe Thr His Tyr Gly Thr Cys Pro Leu Trp Asn Val Phe Glu	
350 355 360 365	
15 acc ttc acc aac ccc ggc caa gtg ctc cgc caa ttc gcg caa atg ccc	1394
Thr Phe Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro	
370 375 380	
20 gac gga cgc aac tac ctg tgg atc tca cgc acc gtg cga cac cac gaa	1442
Asp Gly Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu	
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Ala Arg Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys	
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30 gaa gcg cgc cac gcc gac cgc act gtg tac tcc cgc ggt ttc aac ctc	1538
Glu Ala Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu	
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35 cag gag ctc tcc acc gcc acc ccc atc ggg tcc ggc tgc cga gtg tgc	1586
Gln Asp Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys	
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Ile Asn Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr	
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50 agcttgcttt acgacgcacc ctgcgggggt gggtttacc ttttatgaat gatcagcaat	1743
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	Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu Thr Val Pro			
5	35	40	45	
	Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala Thr Phe Phe			
	50	55	60	
10	Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln Asp Val Met			
	65	70	75	80
	Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln Glu Leu Ser			
	85	90	95	
15	Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met Val Glu Met			
	100	105	110	
20	His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile Ala Val Asp			
	115	120	125	
	Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala Glu Ala Val			
	130	135	140	
25	Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala Arg Gln Asn			
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	Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala Ala Gln Leu			
	165	170	175	
30	Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser Ile Ala Arg			
	180	185	190	
35	Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser Lys Glu Glu			
	195	200	205	
	Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu Leu Thr Ile			
	210	215	220	
40	His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met Ala Thr Glu			
	225	230	235	240
	Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile Val Asp Asp			
	245	250	255	
45	Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile Arg Gly Val			
	260	265	270	
50	Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys Ile Phe His			
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	Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu Gly Gln Leu			
	290	295	300	
55	Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser Thr Leu Gln			
	305	310	315	320
	Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg Val Asp Arg			
	325	330	335	

Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe Thr  
 340 345 350

5 His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe Thr  
 355 360 365

Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly Arg  
 370 375 380

10 Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg Phe  
 385 390 395 400

Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg  
 15 405 410 415

His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu  
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20 Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg Glu  
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